Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 17:15:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013233.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR6013233 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013233.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 17:15:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013233.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,457,933
Mapped reads	2,180,524 / 88.71%
Unmapped reads	277,409 / 11.29%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,598 / 0.76%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	132,379 / 5.39%
Duplication rate	4.46%
Clipped reads	892,308 / 36.3%

2.2. ACGT Content

Number/percentage of A's	41,054,756 / 27.83%
Number/percentage of C's	27,338,069 / 18.53%
Number/percentage of T's	46,850,289 / 31.76%
Number/percentage of G's	32,224,743 / 21.85%
Number/percentage of N's	32,268 / 0.02%
GC Percentage	40.38%

2.3. Coverage

Mean	0.0477

Standard Deviation	0.5444

2.4. Mapping Quality

Mean Mapping Quality	45.8

2.5. Mismatches and indels

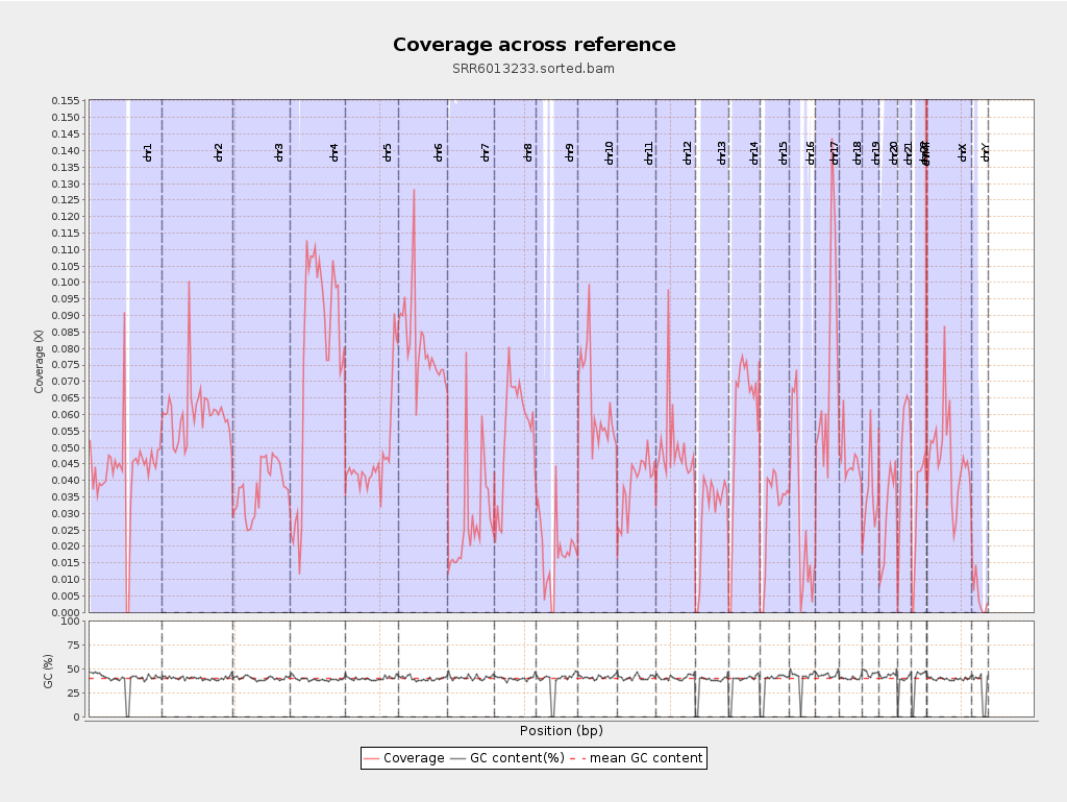
General error rate	0.81%
Mismatches	1,169,529
Insertions	10,253
Mapped reads with at least one insertion	0.47%
Deletions	32,621
Mapped reads with at least one deletion	1.48%
Homopolymer indels	47.81%

2.6. Chromosome stats

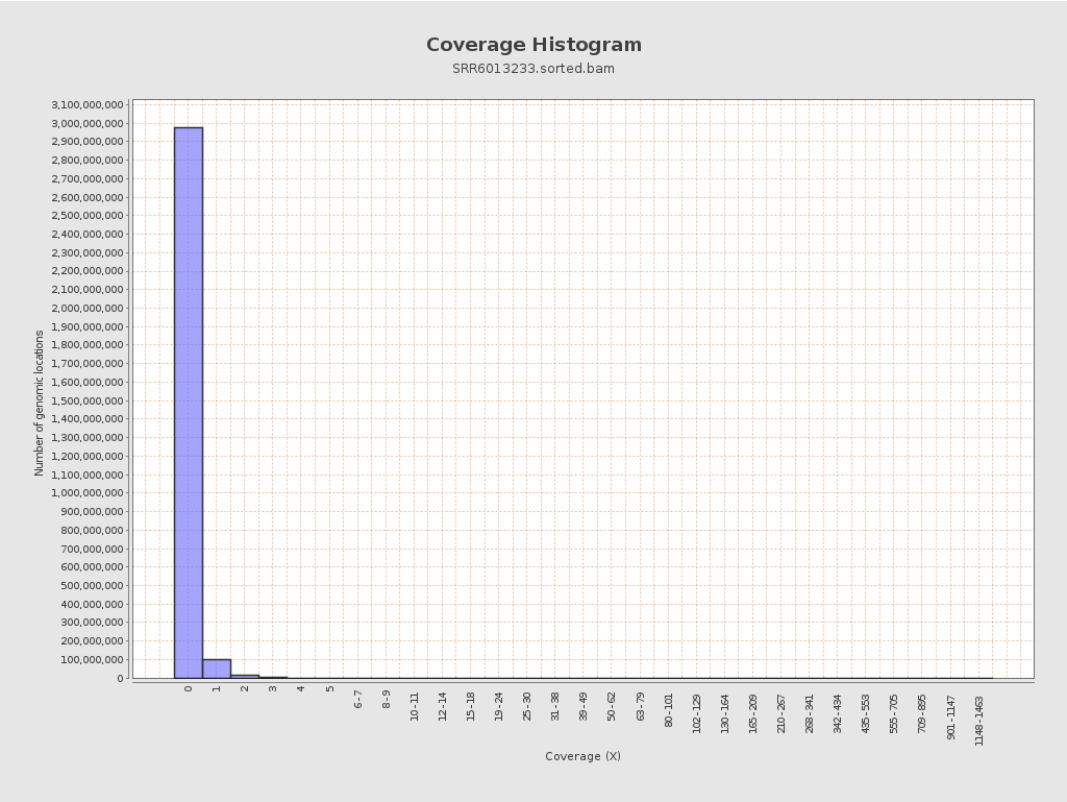
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	10674215	0.0428	1.0146
chr2	243199373	14664885	0.0603	0.5593
chr3	198022430	7513941	0.0379	0.2298
chr4	191154276	14878064	0.0778	0.3437
chr5	180915260	8653864	0.0478	0.2608
chr6	171115067	13963166	0.0816	0.4676
chr7	159138663	4551525	0.0286	0.6272

chr8	146364022	8002999	0.0547	0.8962
chr9	141213431	2540153	0.018	0.3727
chr10	135534747	8623306	0.0636	0.5829
chr11	135006516	5256927	0.0389	0.3504
chr12	133851895	6695426	0.05	0.2729
chr13	115169878	3432739	0.0298	0.2068
chr14	107349540	6255718	0.0583	0.299
chr15	102531392	3111193	0.0303	0.2007
chr16	90354753	2697900	0.0299	0.2527
chr17	81195210	6006261	0.074	0.371
chr18	78077248	3609567	0.0462	0.8289
chr19	59128983	2132505	0.0361	0.6942
chr20	63025520	1871350	0.0297	0.2191
chr21	48129895	2343009	0.0487	0.2702
chr22	51304566	1593541	0.0311	0.2042
chrMT	16571	1030920	62.2123	37.5441
chrX	155270560	7169230	0.0462	0.3012
chrY	59373566	283207	0.0048	0.1124

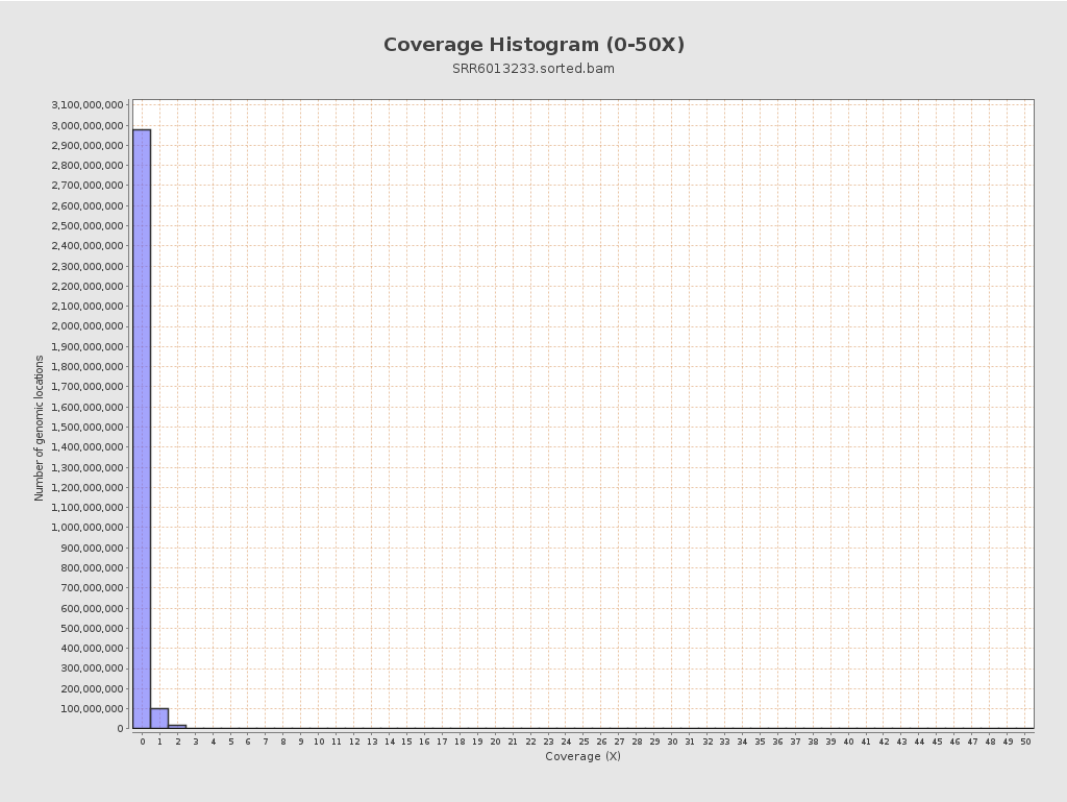
3. Results : Coverage across reference



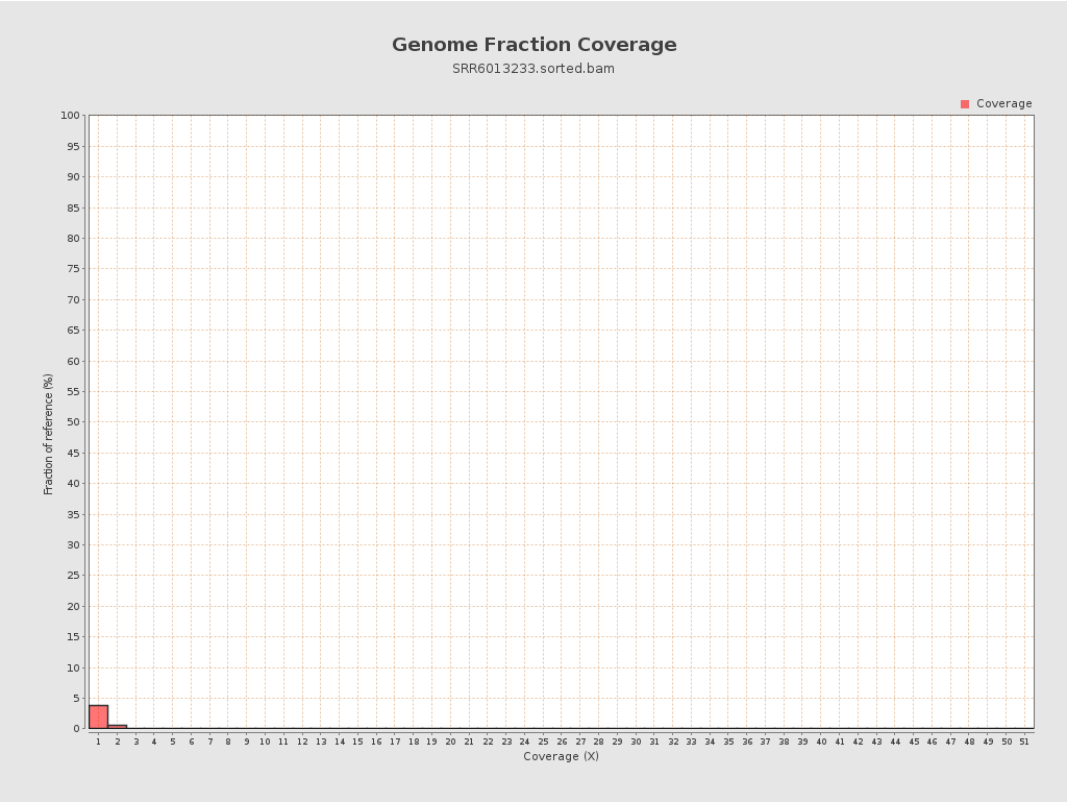
4. Results : Coverage Histogram



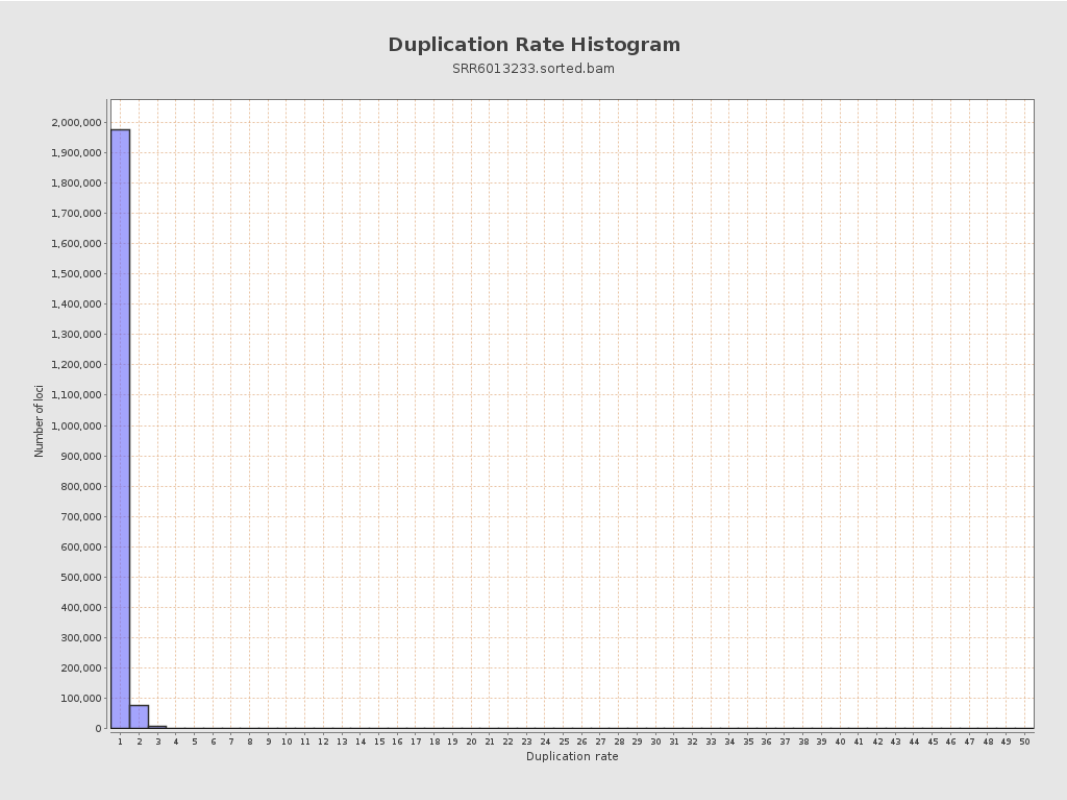
5. Results : Coverage Histogram (0-50X)



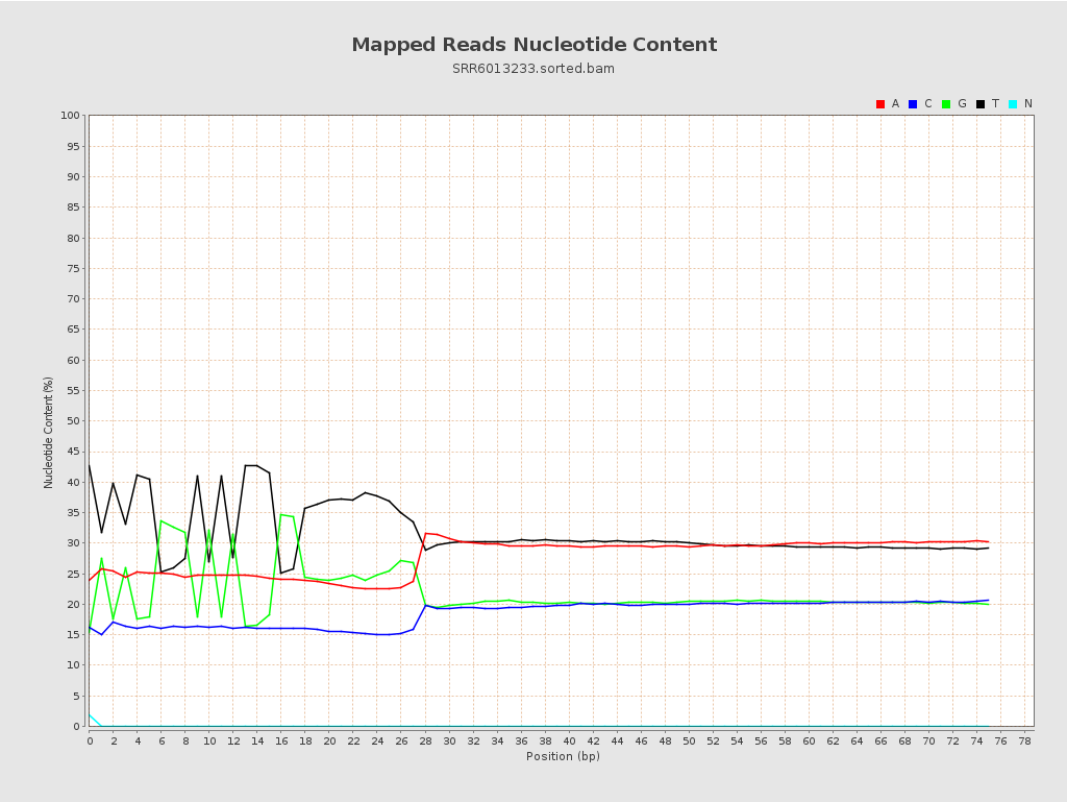
6. Results : Genome Fraction Coverage



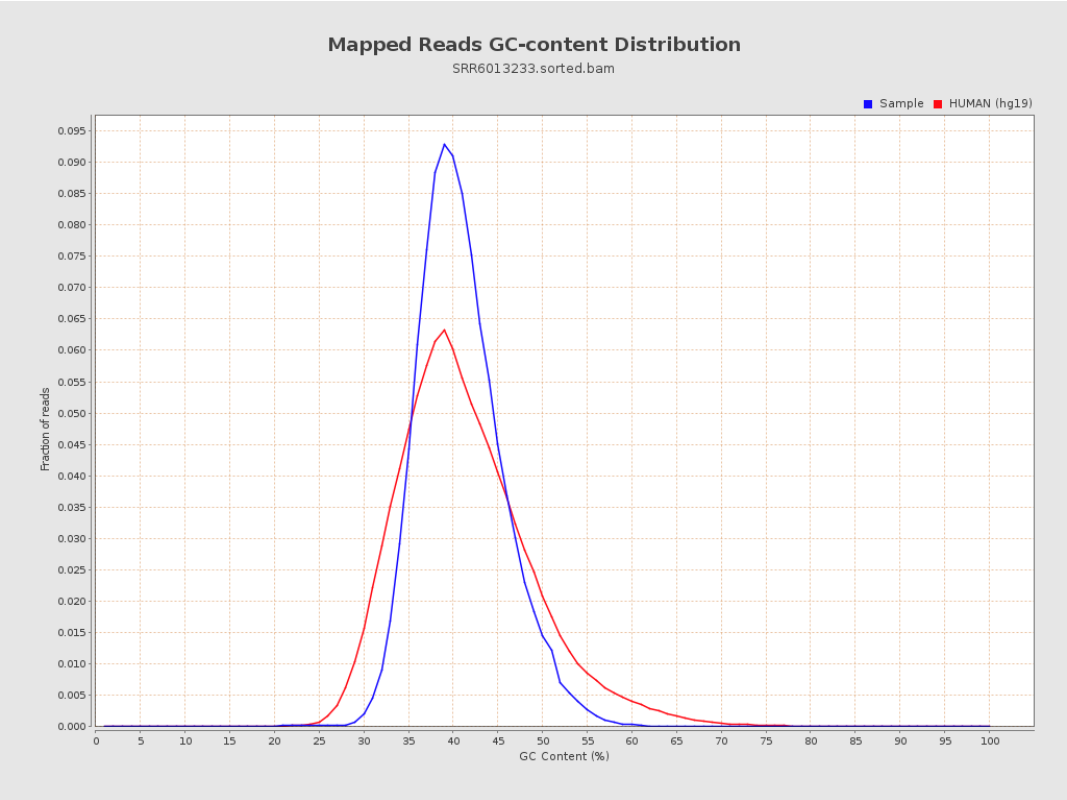
7. Results : Duplication Rate Histogram



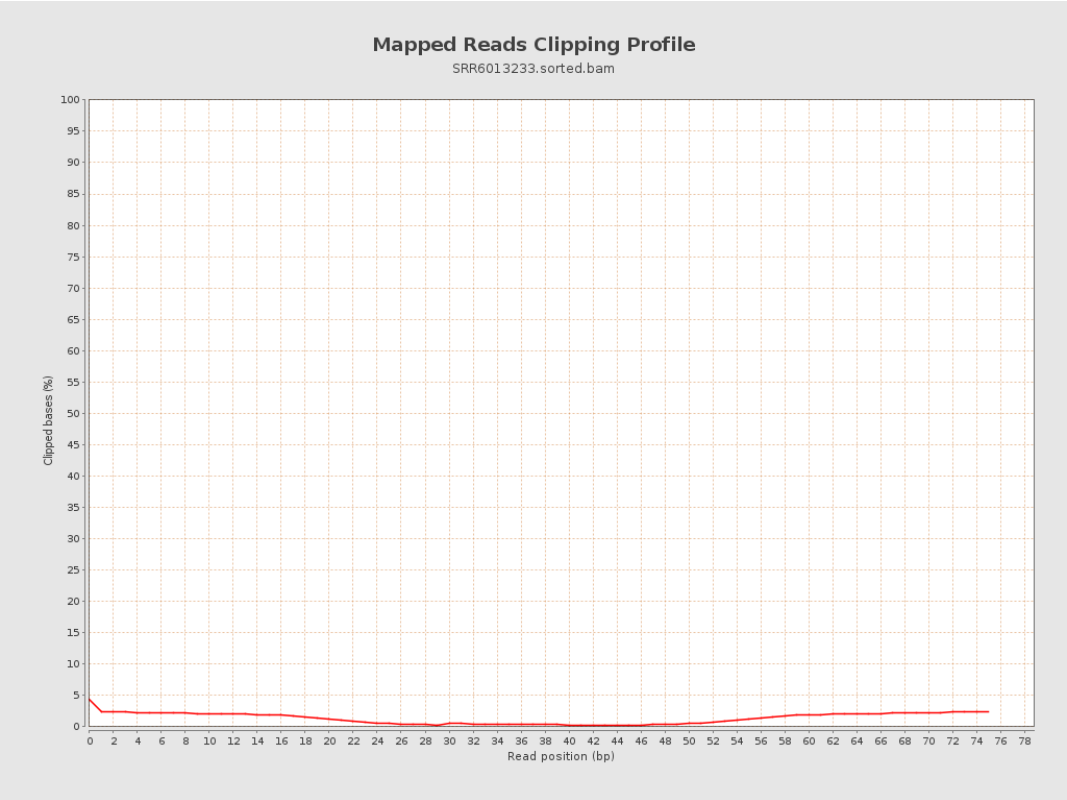
8. Results : Mapped Reads Nucleotide Content



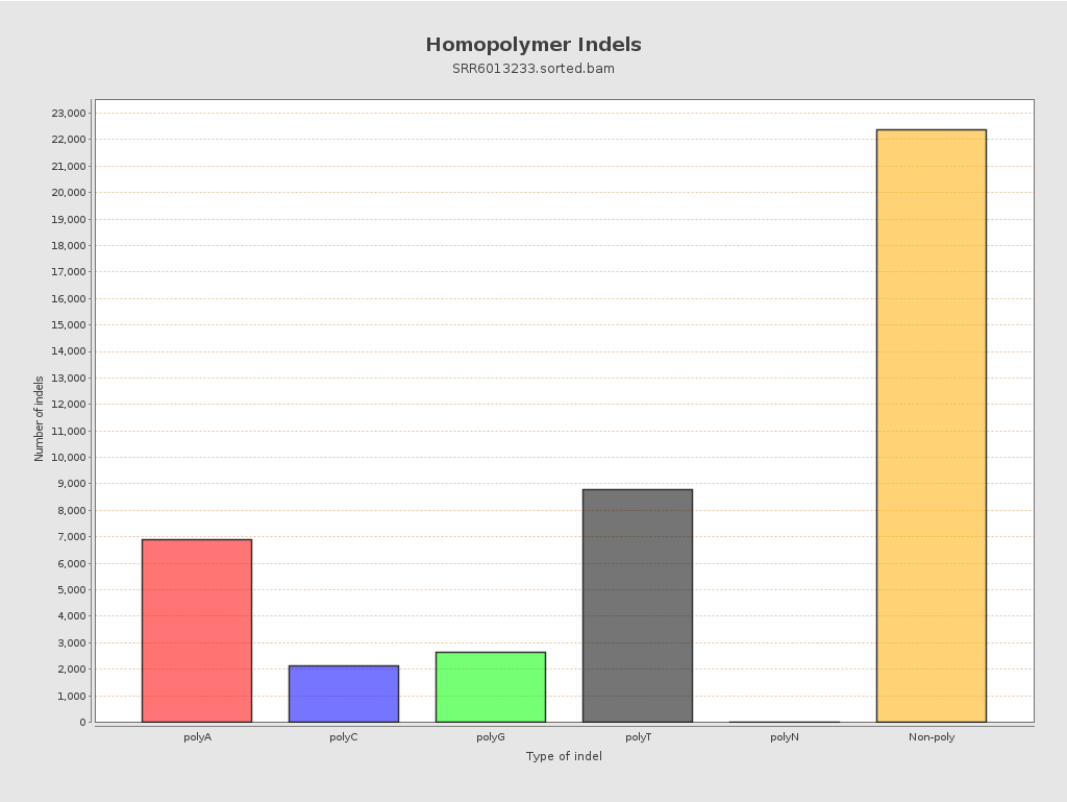
9. Results : Mapped Reads GC-content Distribution



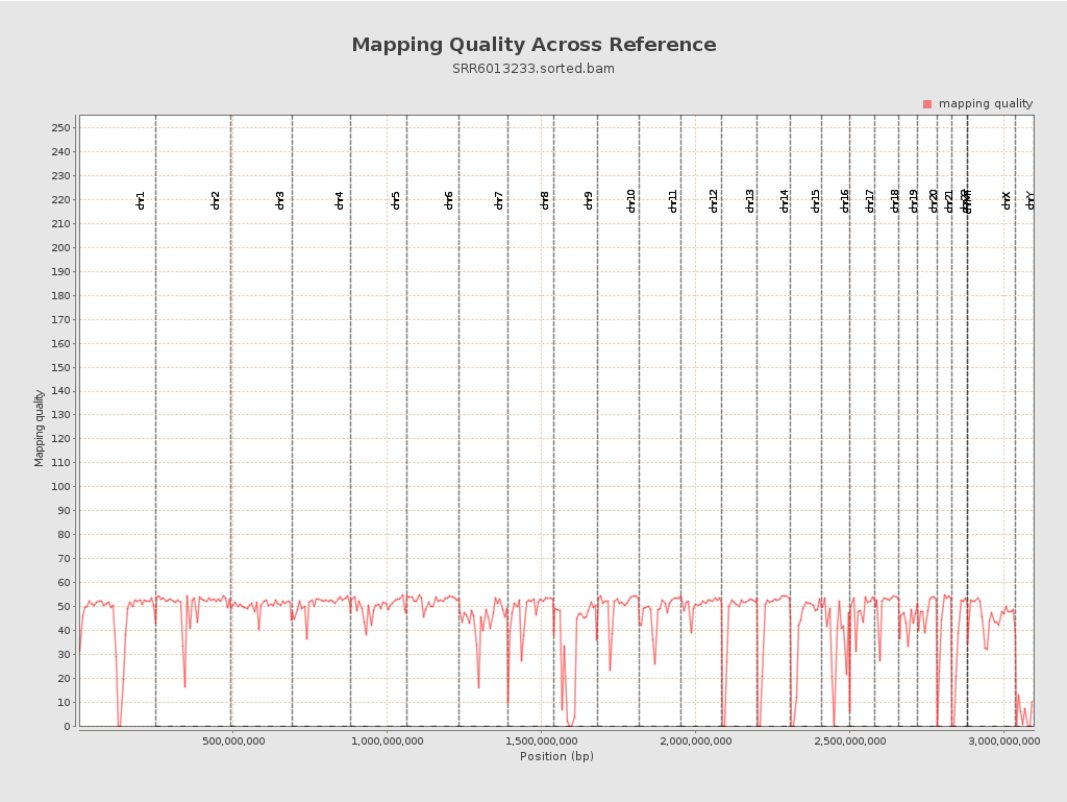
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram